

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 08/88/3090

CRF Processing Date: 9/30/2002
 Edited by: [Signature]
 Verified by: [Signature] (STIC sta: 1644)

ENTERED

1600 #36
 9-30-02

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: Seqs 46 through 54 - deleted extra amino acid number

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TECH CENTER 1600/2900

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/881,509DDATE: 09/30/2002
TIME: 20:37:29

INPUT SET: S36928.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

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SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: SCHENDEL, Dolores J.

(ii) TITLE OF INVENTION: T CELLS SPECIFIC FOR KIDNEY CARCINOMA

(iii) NUMBER OF SEQUENCES: 54

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Arent Fox Kintner Plotkin & Kahn
- (B) STREET: 1050 Connecticut Avenue, Suite 400
- (C) CITY: Washington
- (D) STATE: DC
- (E) COUNTRY: USA
- (F) ZIP: 20036-5339

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/881,509
- (B) FILING DATE: June 24, 1997
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Kitts, Monica Chin
- (B) REGISTRATION NUMBER: 36,105
- (C) REFERENCE/DOCKET NUMBER: 100564-07015

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (202) 857-6000
- (B) TELEFAX: (202) 638-4810

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

RAW SEQUENCE LISTING PATENT APPLICATION US/08/881,509D

DATE: 09/30/2002
TIME: 20:37:29

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47      (ix) FEATURE:
48          (A) NAME/KEY: CDS
49          (B) LOCATION:1..801
50
51      (ix) FEATURE:
52          (A) NAME/KEY: sig_peptide
53          (B) LOCATION:1..54
54
55      (ix) FEATURE:
56          (A) NAME/KEY: mat_peptide
57          (B) LOCATION:55..801
58
59      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
60
61      ATG AGG CAA GTG GCG AGA GTG ATC GTG TTC CTG ACC CTG AGT ACT TTG      48
62      Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu
63      -18          -15          -10          -5
64
65      AGC CTT GCT AAG ACC ACC CAG CCC ATC TCC ATG GAC TCA TAT GAA GGA      96
66      Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly
67          1          5          10
68
69      CAA GAA GTG AAC ATA ACC TGT AGC CAC AAC AAC ATT GCT ACA AAT GAT      144
70      Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp
71      15          20          25          30
72
73      TAT ATC ACG TGG TAC CAA CAG TTT CCC AGC CAA GGA CCA CGA TTT ATT      192
74      Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile
75          35          40          45
76
77      ATT CAA GGA TAC AAG ACA AAA GTT ACA AAC GAA GTG GCC TCC CTG TTT      240
78      Ile Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe
79          50          55          60
80
81      ATC CCT GCC GAC AGA AAG TCC AGC ACT CTG AGC CTG CCC CGG GTT TCC      288
82      Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser
83          65          70          75
84
85      CTG AGC GAC ACT GCT GTG TAC TAC TGC CTC GTG GGT GGT TCT GCA AGG      336
86      Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Gly Ser Ala Arg
87          80          85          90
88
89      CAA CTG ACC TTT GGA TCT GGG ACA CAA TTG ACT GTT TTA CCT GAT ATC      384
90      Gln Leu Thr Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Pro Asp Ile
91          95          100          105          110
92
93      CAG AAC CCT GAC CCT GCC GTG TAC CAG CTG AGA GAC TCT AAA TCC AGT      432
94      Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser
95          115          120          125
96
97      GAC AAG TCT GTC TGC CTA TTC ACC GAT TTT GAT TCT CAA ACA AAT GTG      480
98      Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val
99          130          135          140

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/881,509DDATE: 09/30/2002
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100
101 TCA CAA AGT AAG GAT TCT GAT GTG TAT ATC ACA GAC AAA ACT GTG CTA 528
102 Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu
103 145 150 155
104
105 GAC ATG AGG TCT ATG GAC TTC AAG AGC AAC AGT GCT GTG GCC TGG AGC 576
106 Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser
107 160 165 170
108
109 AAC AAA TCT GAC TTT GCA TGT GCA AAC GCC TTC AAC AAC AGC ATT ATT 624
110 Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile
111 175 180 185 190
112
113 CCA GAA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG 672
114 Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys
115 195 200 205
116
117 CTG GTC GAG AAA AGC TTT GAA ACA GAT ACG AAC CTA AAC TTT CAA AAC 720
118 Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn
119 210 215 220
120
121 CTG TCA GTG ATT GGG TTC CGA ATC CTC CTC CTG AAA GTG GCC GGG TTT 768
122 Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe
123 225 230 235
124
125 AAT CTG CTC ATG ACG CTG CGG CTG TGG TCC AGC TGAGATCTGC AAGATTGTAA 821
126 Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
127 240 245
128
129 GACAGCCTGT GCTCCCTCGC TCCTTCCTCT GCATTGCCCC TCTTCTCCCT CTCCAAACAG 881
130
131 AGGGAACCTCT CCTACCCCCA AGGAGGTGAA AGCTGCTACC ACCTCTGTGC CCCCCCGGCA 941
132
133 ATGCCACCAA CTGGATCCTA CCCGAATTTA TGATTAAGAT TGCTGAAGAG CTGCCAAACA 1001
134
135 CTGCTGCCAC CCCCTCTGTT CCCTTATTGC TGCTTGTCAC TGCCTGACAT TCACGGCAGA 1061
136
137 GGCAAGGCTG CTGCAGCCTC CCCTGGCTGT GCACATTCCC TCCTGCTCCC CAGAGACTGC 1121
138
139 CTCCGCCATC CCACAGATGA TGGATCTTCA GTGGGTTCTC TTGGGCTCTA GGTCCCTGGAG 1181
140
141 AATGTTGTGA GGGGTTTATT TTTTTTTAAT AGTGTTTCATA AAGAAATACA TAGTATTCTT 1241
142
143 CTTCTCAAGA CGTGGGGGGA AATTATCTCA TTATCGAGGC CCTGCTATGC TGTGTGTCTG 1301
144
145 GCGTGTGTGT ATGTCCTGCT GCCGATGCCT TCATTAAAT 1341
146
147
148 (2) INFORMATION FOR SEQ ID NO: 2:
149
150 (i) SEQUENCE CHARACTERISTICS:
151 (A) LENGTH: 267 amino acids
152 (B) TYPE: amino acid

RAW SEQUENCE LISTING
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153 (D) TOPOLOGY: linear
154
155 (ii) MOLECULE TYPE: protein
156 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
157
158 Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu
159 -18 -15 -10 -5
160
161 Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly
162 1 5 10
163
164 Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp
165 15 20 25 30
166
167 Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile
168 35 40 45
169
170 Ile Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe
171 50 55 60
172
173 Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser
174 65 70 75
175
176 Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Gly Ser Ala Arg
177 80 85 90
178
179 Gln Leu Thr Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Pro Asp Ile
180 95 100 105 110
181
182 Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser
183 115 120 125
184
185 Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val
186 130 135 140
187
188 Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu
189 145 150 155
190
191 Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser
192 160 165 170
193
194 Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile
195 175 180 185 190
196
197 Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys
198 195 200 205
199
200 Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn
201 210 215 220
202
203 Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe
204 225 230 235
205

RAW SEQUENCE LISTING PATENT APPLICATION US/08/881,509D

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206 Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
207 240 245
208
209

210 (2) INFORMATION FOR SEQ ID NO: 3:
211

212 (i) SEQUENCE CHARACTERISTICS:

213 (A) LENGTH: 936 base pairs
214 (B) TYPE: nucleic acid
215 (C) STRANDEDNESS: both
216 (D) TOPOLOGY: linear
217

218 (ix) FEATURE:

219 (A) NAME/KEY: CDS
220 (B) LOCATION:1..933
221

222 (ix) FEATURE:

223 (A) NAME/KEY: sig_peptide
224 (B) LOCATION:1..63
225

226 (ix) FEATURE:

227 (A) NAME/KEY: mat_peptide
228 (B) LOCATION:64..933
229

230 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
231

232	ATG GAT ACC TGG CTC GTA TGC TGG GCA ATT TTT AGT CTC TTG AAA GCA	48
233	Met Asp Thr Trp Leu Val Cys Trp Ala Ile Phe Ser Leu Leu Lys Ala	
234	-21 -20 -15 -10	
235		
236	GGA CTC ACA GAA CCT GAA GTC ACC CAG ACT CCC AGC CAT CAG GTC ACA	96
237	Gly Leu Thr Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr	
238	-5 1 5 10	
239		
240	CAG ATG GGA CAG GAA GTG ATC TTG CGC TGT GTC CCC ATC TCT AAT CAC	144
241	Gln Met Gly Gln Glu Val Ile Leu Arg Cys Val Pro Ile Ser Asn His	
242	15 20 25	
243		
244	TTA TAC TTC TAT TGG TAC AGA CAA ATC TTG GGG CAG AAA GTC GAG TTT	192
245	Leu Tyr Phe Tyr Trp Tyr Arg Gln Ile Leu Gly Gln Lys Val Glu Phe	
246	30 35 40	
247		
248	CTG GTT TCC TTT TAT AAT AAT GAA ATC TCA GAG AAG TCT GAA ATA TTC	240
249	Leu Val Ser Phe Tyr Asn Asn Glu Ile Ser Glu Lys Ser Glu Ile Phe	
250	45 50 55	
251		
252	GAT GAT CAA TTC TCA GTT GAA AGG CCT GAT GGA TCA AAT TTC ACT CTG	288
253	Asp Asp Gln Phe Ser Val Glu Arg Pro Asp Gly Ser Asn Phe Thr Leu	
254	60 65 70 75	
255		
256	AAG ATC CGG TCC ACA AAG CTG GAG GAC TCA GCC ATG TAC TTC TGT GCC	336
257	Lys Ile Arg Ser Thr Lys Leu Glu Asp Ser Ala Met Tyr Phe Cys Ala	
258	80 85 90	

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/881,509D

DATE: 09/30/2002
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Line

Error

Original Text